

TTATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT
 1 -----+-----+-----+-----+-----+-----+ 60
 AATAATCCAAAAATGGATGGGTCCTTTTCGGTTGGTTGGAGCTAGAGAACATCTAGACAA
 CTCTAAACGAACCTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC
 61 -----+-----+-----+-----+-----+-----+ 120
 GAGATTTGCTTGAAATTTTAGACACATCGACAGCGAGCCGACGTACGGATCACGTGGATG

 ...

 GTACTATGACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG
 15061 -----+-----+-----+-----+-----+-----+ 15120
 CATGATACTGTTTATCTGTCAAAGTAGTCTTTAATAACTTCAGTTATCGGCGGTGATCTC
 GAGCTACTGTGGTAATTGGAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAAA
 15121 -----+-----+-----+-----+-----+-----+ 15180
 CTCGATGACACCATTAACCTTGTTCTGTTCAAATGCCACCGACCGTATTATACAATTTTT

CANADA first PCR CA
 CTGTTTACAGTGATGTAGAACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACA
 15181 -----+-----+-----+-----+-----+-----+ 15240
 GACAAATGTCCTACATCTTTGAGGTGTGGAATACCCAACCCTAATAGGTTTTACTGT
 GAGCCATGCCTAACATG
 GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA
 15241 -----+-----+-----+-----+-----+-----+ 15300
 CTCGGTACGGATTGTACGAATCCTATTACCGGAGAGACAAGAACGAGCGTTTGTATTGT
 CTTGCTGTAACCTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA
 15301 -----+-----+-----+-----+-----+-----+ 15360
 GAACGACATTGAATAGTGTGGCAAAGATGTCCAATCGATTGCTCACACGCGTTCATAATT

CANADA second PCR TGTAAACCAGGTGGAAC
 GTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTG
 15361 -----+-----+-----+-----+-----+-----+ 15420
 CACTCTACCAGTACACACCGCCGAGTGATATACAATTTGGTCCACCTTGTAGTAGGCCAC
 ATGCTACAACCTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATG
 15421 -----+-----+-----+-----+-----+-----+ 15480
 TACGATGTTGACGAATACGATTATCACAGAAATTGTAAACAGTTCGACAATGTCGGTTAC
 TAAATGCACTTCTTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC
 15481 -----+-----+-----+-----+-----+-----+ 15540
 ATTTACGTGAAGAAAGTTGACTACCATTATTCTATCGACTGTTTCATACAGGCGTTAGATG
 GCGTTAGATG

FIG. 1

AACACAGGCTCTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG
 15541 -----+-----+-----+-----+-----+-----+ 15600
 TTGTCTCCGAGATACTCACAGAGATATCTTTATCCCTACAAGTACTTAAGCACCTAC
 TTGTGTCC CANADA second PCR

 AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTTCTGATGATGCCGTTG
 15601 -----+-----+-----+-----+-----+ 15660
 TCAAAATGCGAATGGACGCATTTGTAAAGAGGTACTACTAAGAAAGACTACTACGGCAAC
 GCGAATGGACGCATTTGTAA CANADA first PCR

 TGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCTAGCATTAAAGAACTTTAAGG
 15661 -----+-----+-----+-----+-----+ 15720
 ACACGATATTGTCATTGATACGCCGAGTTCCAAATCATCGATCGTAATTCTTGAAATTCC

 CAGTTCTTTATTATCAAAATAATGTGTTTCATGTCTGAGGCAAAATGTTGGACTGAGACTG
 15721 -----+-----+-----+-----+-----+ 15780
 GTCAAGAAATAATAGTTTTATTACACAAGTACAGACTCCGTTTTACAACCTGACTCTGAC

 ...

 GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA
 18001 -----+-----+-----+-----+-----+ 18060
 CATCATTCTAGTAATGACCAGAAGTAGGATGTGTCCGTGGATGTGTGGAGTCGCAACTAT

 TAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT
 18061 -----+-----+-----+-----+-----+ 18120
 ATTTCAAGTTCTGACTTCCTAATACACAAGTGTATGGTCCGTATGGTTTCCTGTACTGGA

BNloutS2 ATGAATTACCAAGTCAATGGTTAC
 ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTA
 18121 -----+-----+-----+-----+-----+ 18180
 TGGCATCTGAGTAGAGATACTACCCAAAGTTTTACTTAATGGTTCAGTTACCAATGGGAT

BNlinS GAAGCTATTCGTCACGTTTCG
 ATATGTTTATCACCCGCGAAGAAGCTATTCGTCACGTTTCGTGCGTGGATTGGCTTTGATG
 18181 -----+-----+-----+-----+-----+ 18240
 TATACAAATAGTGGGCGCTTCTTCGATAAGCAGTGCAAGCACGCACCTAACCGAAACTAC

 TAGAGGGCTGTCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGAT
 18241 -----+-----+-----+-----+-----+ 18300
 ATCTCCCGACAGTACGTTGATCTCTACGACACCCATGATTGGATGGAGAGGTCGATCCTA
 GAGGTTCGATCCTA

 TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA
 18301 -----+-----+-----+-----+-----+ 18360
 AAAGATGTCCACAATTGAATCATCGACATGGCTGACCAATACAAGTGTGACTTTTATTGT
 AAAGATGTC BNlinAS
 CATCGACATGGCTGACCAATAC BNloutAS

FIG. 1 cont.

CAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATAC
 18361 -----+-----+-----+-----+-----+-----+ 18420
 GTCTTAAGTGGTCTCAATTACGTTTTGGAGGTGGTCCACTGGTCAAATTTGTAGAATATG

CACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCCTATTAAGATAGTACAAATGCTCA
 18421 -----+-----+-----+-----+-----+-----+ 18480
 GTGAGTACATATTTCCGAACGGGACCTTACATCACGCATAATTCTATCATGTTTACGAGT

...

TACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCC
 28381 -----+-----+-----+-----+-----+-----+ 28440
 ATGGCTTCTCGATGGGCTGCTCAAGCACCACCACTGCCGTTTTACTTTCTCGAGTCGGGG

AGATGGTACTTCTATTACCTAGGAAGTGGCCAGAAAGCTTCACTTCCCTACGGCGCTAAC
 28441 -----+-----+-----+-----+-----+-----+ 28500
 TCTACCATGAAGATAATGGATCCTTGACCGGTCTTCGAAGTGAAGGGATGCCGCGATTG

CIID-28506F AGGCATCGTATGGGTTGCA

CIID-28529T AGGGAGCCTTGAATACACCCAAAGACCA
 AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATT
 28501 -----+-----+-----+-----+-----+-----+ 28560
 TTTCTTCCGTAGCATACCCAACGTTGACTCCCTCGGAAGTTATGTGGGTTTCTGGTGTAA

GGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAAGTTCCCTCAAGGAACAACA
 28561 -----+-----+-----+-----+-----+-----+ 28620
 CCGTGGGCGTTAGGATTATTGTTACGACGGTGGCACGATGTTGAAGGAGTTCCTTGTGT
 TTGTTGT

TTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCC
 28621 -----+-----+-----+-----+-----+-----+ 28680
 AACGGTTTTCCGAAGATGCGTCTCCCTTCGTCTCCGCCGTCAGTTCGGAGAAGAGCGAGG
 AACGGTTTTCCGAAG CIID-28614R

TCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT
 28681 -----+-----+-----+-----+-----+-----+ 28740
 AGTAGTGCATCAGCGCCATTAAGTTCTTTAAGTTGAGGACCGTCGTCATCCCCTTTAAGA

CCTGCTCGAATGGCTAGCGGAGGTGGTGAACTGCCCTCGCGCTATTGCTGCTAGACAGA
 28741 -----+-----+-----+-----+-----+-----+ 28800
 GGACGAGCTTACCGATCGCCTCCACCACTTTGACGGGAGCGCGATAACGACGATCTGTCT

TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAAGGCCAAACTGTC
 28801 -----+-----+-----+-----+-----+-----+ 28860
 AACTTGGTCAACTCTCGTTTCAAAGACCATTTCGGTTGTTGTTGTTCCGGTTTGACAG

CIID-28891F AAGCCTCGCCAAAAACGTAC
 ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAA
 28861 -----+-----+-----+-----+-----+-----+ 28920
 TGATTCTTTAGACGACGACTCCGTAGATTTTTTCGGAGCGGTTTTTGCATGACGGTGTTTT

FIG. 1 cont.

CAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTC
 28921 -----+-----+-----+-----+-----+ 28980
 GTCATGTTGCAGTGAGTTCGTAAACCCTCTGCACCAGGTCTTGTGGGTTCCCTTAAAG

 GGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAA
 28981 -----+-----+-----+-----+-----+ 29040
 CCCCTGGTTCTGGATTAGTCTGTTCCCTTGACTAATGTTTGTAAACCGGCGTTTAACGTGTT

CIID-29074T TCACGCATTGGCATGGAAGTCACAC
 TTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT
 29041 -----+-----+-----+-----+-----+ 29100
 AAACGAGGTTACGGAGACGTAAGAAACCTTACAGTGCGTAACCGTACCTTCAGTGTGGA
 A

 TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTC
 29101 -----+-----+-----+-----+-----+ 29160
 AGCCCTTGTAACCGACTGAATAGTACCTCGGTAATTTAACCTACTGTTTCTAGGTGTAAAG
 AGCCCTTGTAACCGACTGAA CIID-29100R

 AAAGACAACGTCACTACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACA
 29161 -----+-----+-----+-----+-----+ 29220
 TTTCTGTTGCAGTATGACGACTTGTTCTGTGTAAGTGCATGTTTTGTAAAGGGTGGTTGT

 GAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAA
 29221 -----+-----+-----+-----+-----+ 29280
 CTCGGATTTTTCTGTTTTCTTTTTCTGACTACTTCGAGTCGGAAACGGCGTCTCTGTT

 AAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAA
 29281 -----+-----+-----+-----+-----+ 29340
 TTCTTCGTCGGGTGACACTGAGAAGAAGGACGCCGACTGTACCTACTAAAGAGGTCTGTT

CIID-29398F ATG
 CTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAAACACTCATGATG
 29341 -----+-----+-----+-----+-----+ 29400
 GAAGTTTTTAAGGTACTCACCTCGAAGACGACTAAGTTGAGTCCGTATTTGTGAGTACTAC

CIID-29426F AAACGTTTTTCGCAATTCCGT
CIID-29405F CACAAGGCAGATGGGCTATGT
 ACCACACAAGGCACATGG
 ACCACACAAGGCAGATGGGCTATGTAAACGTTTTTCGCAATTCCGTTTACGATACATAGTC
 29401 -----+-----+-----+-----+-----+ 29460
 TGGTGTGTTCCGTCTACCCGATACATTTGCAAAAGCGTTAAGGCAAATGCTATGTATCAG

 TACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAAGTAGGTTTAGTTAACTTTA
 29461 -----+-----+-----+-----+-----+ 29520
 ATGAGAACACGTCTTACTTAAGAGCATTGATTTGTCGTGTTTCATCCAAATCAATTGAAAT

 ATCTCACATAGCAATCTTTAATCAATGTGTAAACATTAGGGAGGACTTGAAAGAGCCACCA
 29521 -----+-----+-----+-----+-----+ 29580
 TAGAGTGTATCGTTAGAAATTAGTTACACATTGTAATCCCTCCTGAACTTTCTCGGTGGT

FIG. 1 cont.

CIID-29584T TTTCATCGAGGCCACGCGGAGTAC
 CATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG
 29581 -----+-----+-----+-----+-----+ 29640
 GTAAAAGTAGCTCCGGTGCGCCTCATGCTAGCTCCCATGTCACTTATTACGATCCCTCTC
 TGTCACTTATTGCGATCCCTCTC
 GTCACTTATTGCGATCCCTCTC
 TGTCACTTATTACGATCCCTCTC
 CTTATTACGATCCCTCTC
 TCCGGTGCGCCTCATGCTAGCT CIID-29592T

 CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG
 29641 -----+-----+-----+-----+-----+ 29700
 GACGGATATACCTTCTCGGGATTACACATTTTAATTAAAATCATCACGATAGGGGTACAC
 G 29618R
 G 29619R
 G 29618-2R
 GACGG CIID-29623R

 ATTTTAATAGCTTCTTAGGAGAATGAC
 29701 -----+-----+----- 29727
 TAAAATTATCGAAGAATCCTCTTACTG

FIG. 1 cont.

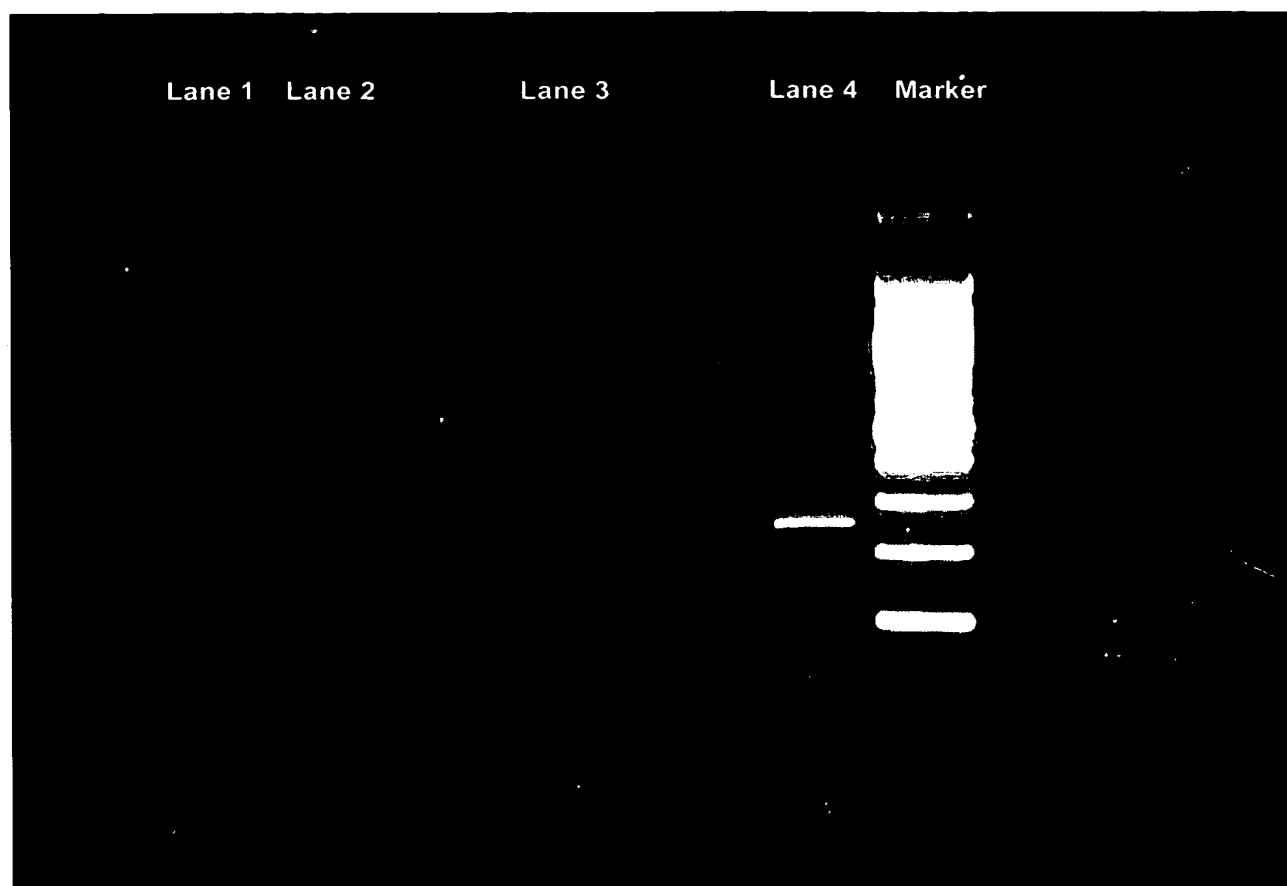


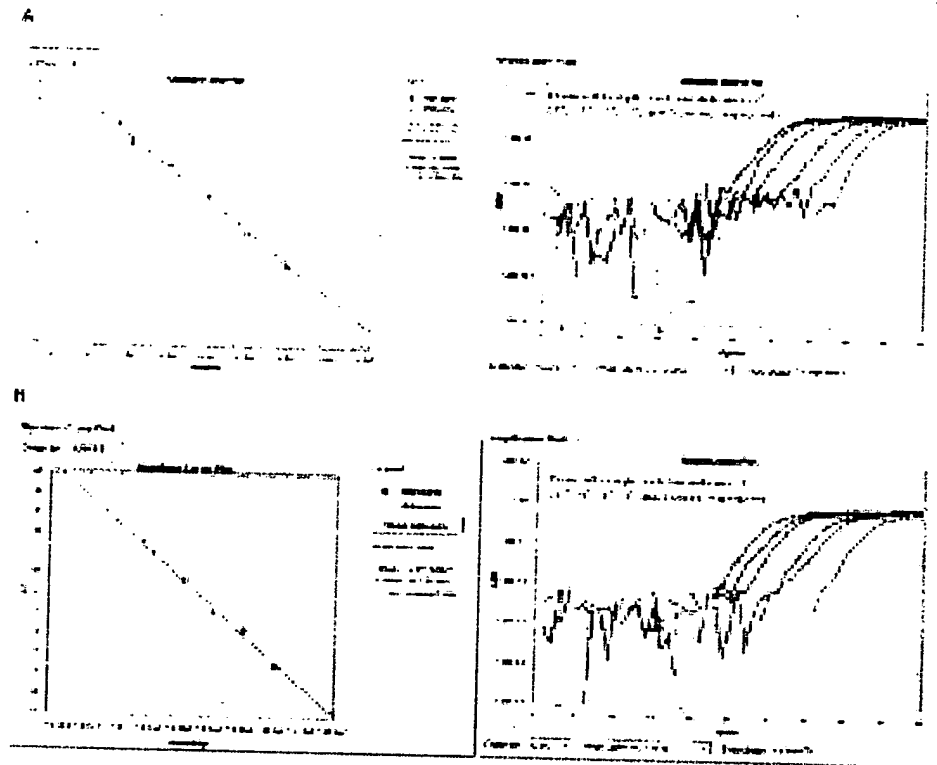
FIG. 2

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AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCACCCGCA
ATCCTAATAACAATGCTGCCACCGTGCTACAACCTCCTCAAGGAACAACATTGCCAAAAGGCTTCT
ACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTAAT
TCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGGAGGTGG
TGAAACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAA
AGGCCAACACAACAAGGCCAAACTGTCTACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTC
GCCAAAAACGTA CTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAA
CAAACCCAAGGAAATTTCTGGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCC
GCAAATTGCACAATTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGT
CACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATT
CAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGC
CTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAAAAGAAGCA
GCCCCTGTGACTCTTCTTCTGCGGCTGACATGGATGATTTCTCCAGACAACCTTCAAAATTCATG
AGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAAGGCAGATGGGC
TATGTAAACGTTTTCTGCAATTCCGTTTACGATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTA
ACTAAACAGCACAAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTAAC
ATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTA
CAGTGAATAATGCTAGGGAGAGC

FIG. 3

FIG. 4



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FIG. 5A

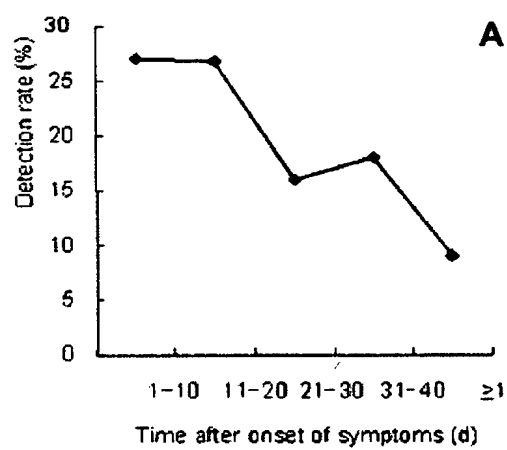


FIG. 5B

